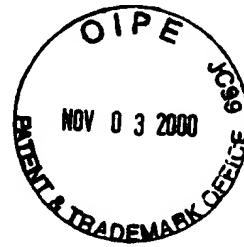


Attachment  
#17

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TECH CENTER 1600/2900



SEQUENCE LISTING

<110> Morell, Andreas  
Imboden, Martin  
Stadler, Beda  
Miescher, Sylvia  
Vogel, Monique  
Amstutz, Hanspeter

<120> POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING  
STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,  
THE DNA ENCODING THEM AND THE PROCESS FOR THEIR  
PREPARATION AND USE

<130> 6816/P63221US0

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NOV 09 2000

TECH CENTER 1600/2900

<140> 09/147,443  
<141> 1999-01-21

<150> PCT/EP97/03253  
<151> 1997-06-20

<150> EP 96810421.6  
<151> 1996-06-24

<160> 77

<170> PatentIn Ver. 2.1

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Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat 96  
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr  
20 25 30

gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca ggt ata tgg ttt gat gga agt aac aaa aac tat gca gac tcc gtg 192  
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat tgt 288  
Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac tac atg 336
Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Tyr Met
          100           105           110

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gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc cca  
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro  
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          1           5           10          15

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20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
       65              70              75              80

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met  
                  100                 105                 110

Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Pro
							115					125
									120			

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<212> DNA  
<213> Homo sapiens
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Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1           5           10          15

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gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
           20                  25                  30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ttg ctg atc tat ggt	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly	
35	40
	45
gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60
tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat	240
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
65	70
	75
	80
ttt gca act tac tac tgt caa gag agt tac agt aat cct cta atc acc	288
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr	
85	90
	95
ttc ggc caa ggg aca cga ctg gag act aaa	318
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys	
100	105

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	10
	15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn	
20	25
	30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr Gly	
35	40
	45
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50	55
	60
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
65	70
	75
	80
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr	
85	90
	95
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys	
100	105

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 <212> DNA  
 <213> Homo sapiens

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 <222> (1)...(375)

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1				5					10				15			
tcc	ctg	aga	ctc	tcc	tgt	gaa	gcg	tct	gga	ttc	gcc	ctc	aga	agt	tct	96
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Ala	Leu	Arg	Ser	Ser	
	20							25					30			
ggc	atg	cac	tgg	gtc	cgc	cag	gct	cct	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
	35							40				45				
gca	ctt	ata	tgg	ttt	gat	gga	agt	atc	aga	tcg	tat	gca	gaa	tcc	gtg	192
Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
	50							55			60					
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	act	tcc	aag	aac	acc	cta	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
	65							70			75			80		
ctc	caa	atg	cgc	agt	ctg	agt	gcc	gac	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Arg	Ser	Leu	Ser	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
		85						90			95					
gcg	aga	gac	aag	gcg	gtt	cgg	gga	att	agc	agg	tac	aac	tat	tac	atg	336
Ala	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
		100						105			110					
gac	gtc	tgg	ggc	aaa	ggg	acc	acg	gtc	acc	gtc	tcc	tca				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115						120			125					

<210> 6  
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 <212> PRT  
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<400> 6																
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
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	20							25				30				
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
	35							40			45					
Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
		50						55			60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
	65							70			75			80		
Leu	Gln	Met	Arg	Ser	Leu	Ser	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
		85						90			95					
Ala	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
		100						105			110					
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(318)

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1 5 10 15	

gtc acc atc act tgc cg gca agt cag aac att atc cgc tat tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn	
20 25 30	

tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	
35 40 45	

gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	

tct ggg aca gat ttc act ctc acc atc agt agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr	
85 90 95	

ttc ggc cct ggg acc aaa gtg gag atc aaa	318
Phe Gly Pro Gly Thr Lys Val Glu Ile Lys	
100 105	

<210> 8  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	8
1 5 10 15	

Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn	8
20 25 30	

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	8
35 40 45	

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	8
50 55 60	

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	8
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65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr  
85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 9  
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<213> Homo sapiens

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Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96  
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192  
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288  
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336  
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 10  
<211> 125  
<212> PRT  
<213> Homo sapiens

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1 5 10 15

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 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
 100 105 110  
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

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 <212> DNA  
 <213> Homo sapiens

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 1 5 10 15  
 gtc acc atc acc tgc cgg gca agt cag agt atc atc agg tat ttg aat 96  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
 20 25 30  
 tgg tat cag cac aaa cca gga aaa gcc cct aaa ctc ctc atc ttt gct 144  
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala  
 35 40 45  
 gca tcg aat ttg caa act ggg gtc cca tcc agg ttc agt ggc agt gga 192  
 Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 50 55 60  
 tct ggg aca gat ttc act ctc acc atc agt gac ctg cag cct gag gat 240  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp  
 65 70 75 80  
 ttc gca act tac tac tgt caa cag agt tac agt agg ccg ttc act ttt 288  
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe  
 85 90 95  
 ggc cgg ggg acc agc ctg gac atc aaa 315  
 Gly Arg Gly Thr Ser Leu Asp Ile Lys  
 100 105

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 <212> PRT  
 <213> Homo sapiens

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   20                 25   30  
  
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala  
   35                 40   45  
  
 Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
   50                 55   60  
  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp  
   65                 70   80  
  
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe  
   85                 90   95  
  
 Gly Arg Gly Thr Ser Leu Asp Ile Lys  
   100                 105

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 <212> DNA  
 <213> Homo sapiens

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 <222> (1)..(375)

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 tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat   96  
 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr  
   20                 25   30  
  
 gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg   144  
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
   35                 40   45  
  
 gca ggt ata tgg ttt gat gga agc aac aaa aac tat gca gac tcc gtg   192  
 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
   50                 55   60  
  
 aag ggc cga ttc acc atc tcc aga gac aac tcc aag aac act ctg ttt   240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe  
   65                 70   80

ctg cac atg aac agc ctg aga gcc gag gac acg gct aca tat tac tgt 288  
Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95

gcg aga gag agg gcg att cgg gga atc agt aga tac aat tac tac atg 336  
Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375  
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20 25 30

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35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe  
65 70 75 80

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

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<222> (1) .. (315)

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Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att cga agc tct tta aat 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn

20

25

30

tgg tat cag cag aaa cca ggg aaa gcc cct aaa gtc ctg atc tat gct      144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala  
35                          40                          45

gca tcc agt ttg caa agt ggg gtc cca tcc agg ttc agt ggc aga gga      192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly  
50                          55                          60

tct ggg aca gat ttc act ctc acc atc agc agt ctg cag cct gaa gat      240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65                          70                          75                          80

ttt gcg act tat tat tgt caa cag agt tcc agt tcc tcg tgg acg ttc      288  
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe  
85                          90                          95

ggc caa ggg acc aag gtg gaa atc aaa      315  
Gly Gln Gly Thr Lys Val Glu Ile Lys  
100                          105

&lt;210&gt; 16

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1                          5                          10                          15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn  
20                          25                          30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala  
35                          40                          45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly  
50                          55                          60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65                          70                          75                          80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe  
85                          90                          95

Gly Gln Gly Thr Lys Val Glu Ile Lys  
100                          105

&lt;210&gt; 17

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(378)

<400> 17

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Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys	
1			5						10					15		

tcc ctg aga ctt tcc tgt gca gcg tct gga ttc agt ttc aat agc cat 96

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Asn	Ser	His	
			20					25				30				

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
			35				40				45					

gca ttt ata tgg ttt gat ggc agt aat aaa tac tat gca gac tcc gtg 192

Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
			50			55			60							

aag ggc cga ttc acc atc acc aga gac aac tcc aag aac acg ctg tat 240

Lys	Gly	Arg	Phe	Thr	Ile	Thr	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
			65			70			75			80				

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					85			90			95					

gcg aga gag acc tca gta agg cta ggg tat agc cgc tac aat tac tac 336

Ala	Arg	Glu	Thr	Ser	Val	Arg	Leu	Gly	Tyr	Ser	Arg	Tyr	Asn	Tyr	Tyr	
					100			105			110					

atg gac gtc tgg ggc aaa ggg acc acg gtc acc atc tcg tca 378

Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Ile	Ser	Ser			
			115				120			125						

<210> 18

<211> 126

<212> PRT

<213> Homo sapiens

<400> 18

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys		
1			5						10			15				

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His 30

			20				25			30						
--	--	--	----	--	--	--	----	--	--	----	--	--	--	--	--	--

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45

			35				40			45						
--	--	--	----	--	--	--	----	--	--	----	--	--	--	--	--	--

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 60

			50				55			60						
--	--	--	----	--	--	--	----	--	--	----	--	--	--	--	--	--

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80

			65				70			75			80			
--	--	--	----	--	--	--	----	--	--	----	--	--	----	--	--	--

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95

			85				90			95						
--	--	--	----	--	--	--	----	--	--	----	--	--	--	--	--	--

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 110

			100				105			110						
--	--	--	-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser  
115 120 125

<210> 19  
<211> 318  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(318)

<400> 19  
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15  
  
gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
20 25 30  
  
tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45  
  
gca tcc agt ttg caa ggt ggg gtc cca tca agg ttc agt ggc agt gga 192  
Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60  
  
tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80  
  
ttt gca act tat tac tgt caa cag agt tac agg gcc cct cag tgg acg 288  
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr  
85 90 95  
  
ttc ggc caa ggg acc aag gtg gaa atc aaa 318  
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 20  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 20  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15  
  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn  
20 25 30  
  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45  
  
Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr  
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 21

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(375)

<400> 21

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
65 70 75 80

ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gag aag gcg ctt cgg gga atc agc aga tac aac tat tac ctg 336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 22

<211> 125

<212> PRT

<213> Homo sapiens

<400> 22

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
 100 105 110  
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

<210> 23  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(333)

<400> 23

gtg	gtg	act	cag	cca	ccc	tca	gcg	tct	ggg	acc	ccc	gga	cag	agg	gtc		48
Val	Val	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val		
1	5							10					15				

acc	atc	tct	tgt	tct	gga	agc	aac	tcc	atc	ctt	gga	agt	aag	tat	gtt		96
Thr	Ile	Ser	Cys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Gly	Ser	Lys	Tyr	Val		
20	25								30								

tac	tgg	tac	cag	aaa	ctc	cca	gga	acg	gcc	ccc	aaa	ctc	ctc	atc	tat		144
Tyr	Trp	Tyr	Gln	Lys	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr		
35	40								45								

aag	aat	gat	cag	ccc	tca	ggg	gtc	tct	gac	cga	ttc	tct	ggc	tcc		192	
Lys	Asn	Asp	Gln	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser		
50	55								60								

aag	tct	ggc	acc	tcc	gcc	ctg	gcc	atc	agt	ggg	ctc	cgg	tcc	gag		240	
Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Arg	Ser	Glu		
65	70							75					80				

gat	gag	gct	gac	tat	tac	tgt	gca	cca	tgg	gat	gcc	aac	ctg	ggt	ggc		288
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Pro	Trp	Asp	Ala	Asn	Leu	Gly	Gly		
85	90								95								

ccg	gtg	tcc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	agt	cag	ccc		333
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----

Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
100 105 110

<210> 24  
<211> 111  
<212> PRT  
<213> Homo sapiens

<400> 24  
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val  
1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val  
20 25 30

Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr  
35 40 45

Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser  
50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu  
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly  
85 90 95

Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro  
100 105 110

<210> 25  
<211> 375  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(375)

<400> 25  
cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96  
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192  
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

65	70	75	80	
ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys				288
85		90		95
gcg aga gac aag gcg gtt cg <sup>g</sup> gga att agc agg tac aac tat tac atg Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met				336
100		105		110
gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser				375
115		120		125
 <b>&lt;210&gt; 26</b>				
<b>&lt;211&gt; 125</b>				
<b>&lt;212&gt; PRT</b>				
<b>&lt;213&gt; Homo sapiens</b>				
 <b>&lt;400&gt; 26</b>				
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly				
1	5	10	15	
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser				
20		25		30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val				
35		40		45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val				
50		55		60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr				
65		70		75
80		85		90
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys				
95		100		105
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met				
110		115		120
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser				
125		130		135
 <b>&lt;210&gt; 27</b>				
<b>&lt;211&gt; 312</b>				
<b>&lt;212&gt; DNA</b>				
<b>&lt;213&gt; Homo sapiens</b>				
 <b>&lt;220&gt;</b>				
<b>&lt;221&gt; CDS</b>				
<b>&lt;222&gt; (1) .. (312)</b>				
 <b>&lt;400&gt; 27</b>				
gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga				
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg				
1	5	10	15	48

gtc acc atc act tgc cgg aca agt cag acc att agc aga aat tta aat 96  
Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn  
20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

aca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192  
Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

tct ggg aca gat ttc act ctc acc atc aat agt cta caa cct gaa gat 240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp  
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc cct tcg ttc ggc 288  
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly  
85 90 95

caa ggg acc aag gtg gaa atc aaa 312  
Gln Gly Thr Lys Val Glu Ile Lys  
100

<210> 28

<211> 104

<212> PRT

<213> Homo sapiens

<400> 28

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr Ala  
35 40 45

Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly  
85 90 95

Gln Gly Thr Lys Val Glu Ile Lys  
100

<210> 29

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(375)

<400> 29  
cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtc cag ccg ggg ggg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
  
tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30  
  
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
  
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60  
  
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg ctc tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr  
65 70 75 80  
  
ctg caa atg aat agc ctg aga gcc gag gac acg gct gta tat tat tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
  
gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110  
  
gac gtc tgg ggc aag ggg gcc acg gtc acc gtc tcc tca 375  
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser  
115 120 125

<210> 30

<211> 125

<212> PRT

<213> Homo sapiens

<400> 30

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu

100

105

110

Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser  
115 120 125

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<210> 31  
<211> 318  
<212> DNA  
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) .. (318)

<400> 31  
gtg atg acc cag tct cca tcc tcc ctg tct gca tct ata ggc gac aga 48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
1 5 10 15

tgg tat cag cag aaa cca ggg aaa gcc cct agg ctc cta atc ttt gct 144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala  
35 40 45

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gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
      50          55          60

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tct ggg aca gat ttc acc ctc acc atc agc agt ctg caa cct gag gat 240  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
     65                70                75                80

ttt gga act tac tac tgt caa cag aat tac agg acc cct cag tgg acg 288  
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr  
85 90 95

ttc ggc caa ggg acc aag gta gaa atc aaa  
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 32  
<211> 106  
<212> PRT  
<213> *Homo sapiens*

<400> 32  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala  
35 40 45

Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly
50						55								60	
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
65					70						75				80
Phe	Gly	Thr	Tyr	Tyr	Cys	Gln	Gln	Asn	Tyr	Arg	Thr	Pro	Gln	Trp	Thr
85								90							95
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys						
100								105							

<210> 33  
<211> 378  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (1) .. (378)

<400> 33  
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96  
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
                  20                 25                 30

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ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg      144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

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gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
      50          55                  60

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aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
   65           70           75           80

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ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tat 288  
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr  
85 90 95

tgt gcg aga gag aag gcg ctt cg<sup>g</sup> gga atc agc aga tac aac tat tac 336  
 Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr  
                   100                  105                  110

<210> 34  
<211> 126  
<212> PRT  
<213> *Homo sapiens*

<400> 34  
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr  
 85 90 95  
 Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr  
 100 105 110  
 Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

<210> 35  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1)...(333)  
  
 <400> 35  
 gtg gtg act cag gag ccc tca ctg act gtg tcc cca gga ggg aca gtc 48  
 Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val  
 1 5 10 15  
 act ctc acc tgt gct tcc agc act ggg gca gtc acc agg ggt tac tat 96  
 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr  
 20 25 30  
 cca aac tgg ttc cag cag aag cct gga caa gca ccc agg gca ctg att 144  
 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile  
 35 40 45  
 tat agt aca aac aaa aaa cac tcc tgg acc cct gcc cggt ttc tca ggc 192  
 Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly  
 50 55 60  
 tcc ctc ctt ggg ggc aaa gct gcc ctg aca ctg tca ggt gtg cag cct 240  
 Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro  
 65 70 75 80  
 gaa gac gag gct gaa tat tac tgc ctg ctc tac tat ggt ggt gct caa 288  
 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln  
 85 90 95

ctc gta ttc ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc 333  
 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro  
                   100                  105                  110

<210> 36  
<211> 111  
<212> PRT  
<213> *Homo sapiens*

<400> 36  
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val  
1 5 10 15

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr  
20 25 30

Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile  
35 40 45

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro  
65 70 75 80

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln  
                   85                  90                  95

Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro  
                  100                 105                 110

<210> 37  
<211> 375  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (1) . . (375)

<400> 37  
cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg  
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15 48

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96  
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
                   20                  25                  30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192  
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
       50                 55                 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288  
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336  
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 38

<211> 125

<212> PRT

<213> Homo sapiens

<400> 38

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 39

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (315)

<400> 39

gtg ttg acc cag tct cca tcc tcc ctg tct gca tct ata cga gac aga 48  
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg

1	5	10	15	
gtc acc atc act tgc cgg gca agt cag aac att ggc agt tat tta aat				96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn				
20	25	30		
tgg tat cag cac aaa cca ggg aca gcc cct aaa ctc ctg atc tat gct				144
Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala				
35	40	45		
gta tcc gct ttg caa agt ggg gtc cca tcg agg ttc agt ggc agt aga				192
Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg				
50	55	60		
tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat				240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp				
65	70	75	80	
ttt gca act tac tac tgt caa cag agt tac agt ccc ccg tac act ttc				288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe				
85	90	95		
ggc cag ggg acc aac ctg cag atc aaa				315
Gly Gln Gly Thr Asn Leu Gln Ile Lys				
100	105			
<210> 40				
<211> 105				
<212> PRT				
<213> Homo sapiens				
<400> 40				
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg				
1	5	10	15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn				
20	25	30		
Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala				
35	40	45		
Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg				
50	55	60		
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp				
65	70	75	80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe				
85	90	95		
Gly Gln Gly Thr Asn Leu Gln Ile Lys				
100	105			
<210> 41				
<211> 375				
<212> DNA				
<213> Homo sapiens				

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<220>
<221> CDS
<222> (1)..(375)

<400> 41
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Leu Glu Trp Val
35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gag aag gcg gtt cg gga att agt aga tac aac tac tac atg 336
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 42
<211> 125
<212> PRT
<213> Homo sapiens

<400> 42
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 48
1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 43

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(315)

<400> 43

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gtg gga gac aga 48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att atc aac aat tta aat 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn  
20 25 30

tgg tat cag cag aaa cca ggc aaa gcc cct gaa ctc ctg atc tat gct 144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Ile Tyr Ala  
35 40 45

gca tcc agt ttg caa agt ggg gtc cct tca agg ttc cgt ggc agt gga 192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly  
50 55 60

tct ggg aga gat ttc act ctc acc gtc acc agt ctg caa cct gaa gat 240  
Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp  
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc ctg tgg acg ttc 288  
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe  
85 90 95

ggc caa ggg acc aag gtg gaa atc aaa 315  
Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 44

<211> 105

<212> PRT

<213> Homo sapiens

<400> 44

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala

35

40

45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly  
 50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp  
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe  
 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

&lt;210&gt; 45

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(375)

&lt;400&gt; 45

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48  
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96  
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192  
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt 288  
 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336  
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
 100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375  
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

&lt;210&gt; 46

&lt;211&gt; 125

<212> PRT

<213> Homo sapiens

<400> 46  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15  
  
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr  
20 25 30  
  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
  
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50 55 60  
  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
  
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100 105 110  
  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 47

<211> 315

<212> DNA

<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(315)  
  
<400> 47  
gtg atg acc cag tct cca ttc tcc ctg tct gca tct gta gga gac aga 48  
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15  
  
gtc acc atc act tgc cgg gca agt cag aac att agg agt ttt tta agt 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser  
20 25 30  
  
tgg tat cag cag aaa cca ggg aca gcc cct aag ctc ctg atc tat gct 144  
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45  
  
gca tcc agg ttg caa agt ggg gtc cca tca agg ttc agt ggc agt ggg 192  
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60  
  
tct ggg aca gat ttc act ctc acc atc agc act ctg caa cct gaa gat 240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp  
65 70 75 80  
  
ttt gcg act tac tac tgt caa cag agt tac agt gcc cct tgg acg ttc 288

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe	85	90	95	
ggc caa ggg acc aag ctg gaa atc aaa				315
Gly Gln Gly Thr Lys Leu Glu Ile Lys				
100		105		
<210> 48				
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<212> PRT				
<213> Homo sapiens				
<400> 48				
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg				
1	5	10	15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser				
20	25	30		
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala				
35	40	45		
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly				
50	55	60		
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp				
65	70	75	80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe				
85	90	95		
Gly Gln Gly Thr Lys Leu Glu Ile Lys				
100		105		
<210> 49				
<211> 375				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (1)..(375)				
<400> 49				
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg				48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly				
1	5	10	15	
tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc tcc agg agt tat				
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr				
20	25	30		
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg				144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val				
35	40	45		
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg				192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val				

50	55	60	
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aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat      240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                    70                    75                    80

ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt      288  
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85                    90                    95

gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg      336  
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100                 105                 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca      375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115                 120                 125

<210> 50  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 50  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1                 5                 10                 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr  
20                 25                 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35                 40                 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val  
50                 55                 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                 70                 75                 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85                 90                 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu  
100                 105                 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115                 120                 125

<210> 51  
<211> 315  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(315)

<400> 51

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Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
gtc acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn	
20 25 30	
tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
ttt gca act tac tac tgt caa cag agt tac agt acc cga ttc act ttc	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe	
85 90 95	
ggc cct ggg acc aaa gtg gat atc aaa	315
Gly Pro Gly Thr Lys Val Asp Ile Lys	
100 105	

<210> 52  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 52	
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn	
20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe	
85 90 95	
Gly Pro Gly Thr Lys Val Asp Ile Lys	
100 105	

<210> 53  
 <211> 384  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(384)

<400> 53

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

tcc ctg aga ctt tcc tgt gca gcg tct gga ttt acc ttc agt agc tat 96  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gca gat ata tgg ttt gat gga ggt aat aaa cat tat gca gac ttc gtg 192  
Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val  
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg gtg tat 240  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  
65 70 75 80

cta caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt 288  
Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg agg gat tac tat agc gtt act aag aaa ctc aga ctc cac tac tac 336  
Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr  
100 105 110

tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 384  
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 54

<211> 128

<212> PRT

<213> Homo sapiens

<400> 54

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr  
100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 55

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(315)

<400> 55

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48  
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat tta acc 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr  
20 25 30

tgg tat cag caa aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144  
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

gca tcc aat tta caa agt ggg gtc cca tca agg ttc agc ggc agt gga 192  
Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

tct ggc aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat 240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

ttt gca act tat tac tgt cta caa gat aac aat ttc ccg tac act ttt 288  
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe  
85 90 95

ggc cag ggg acc aag ctg gag atc aaa 315  
Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 56

<211> 105

<212> PRT

<213> Homo sapiens

<400> 56

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr  
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala  
35 40 45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe  
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 57

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (375)

<400> 57

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48  
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375  
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 58  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 58  
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
1 5 10 15  
  
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
20 25 30  
  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
  
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val  
50 55 60  
  
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
  
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
  
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  
100 105 110  
  
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Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
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gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat 96  
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
20 25 30  
  
tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat act 144  
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr  
35 40 45  
  
gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192  
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60  
  
tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240  
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288  
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
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ggc cag ggg acc aag ctg cag atc aaa 315  
Gly Gln Gly Thr Lys Leu Gln Ile Lys  
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<213> *Homo sapiens*

<400> 60  
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1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
                   20                  25                  30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr  
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
65                   70                   75                   80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
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Gly Gln Gly Thr Lys Leu Gln Ile Lys  
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1 5 10 15

tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt . 96  
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe  
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ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            35          40          45

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gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt		192	
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val			
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aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat		240	
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt		288	
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
gcg aga gag aag gcg gtt cg <sup>g</sup> gga att agt aga tac aac tac tac atg		336	
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met			
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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser			
115	120	125	
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Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe			
20	25	30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met			
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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser			
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 gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat 96  
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn  
 20 25 30  
  
 tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat gct 144  
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala  
 35 40 45  
  
 gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192  
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val  
 50 55 60  
  
 tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240  
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp  
 65 70 75 80  
  
 ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288  
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe  
 85 90 95  
  
 ggc cag ggg acc aag ctg cag atc aaa 315  
 Gly Gln Gly Thr Lys Leu Gln Ile Lys  
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Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
   20          25          30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
   35          40          45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
   50          55          60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
   65          70          75          80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
   85          90          95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
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gtccaggtgg aggtgcagct gctcgagtct gg 32

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<400> 71  
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<400> 72  
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<210> 75  
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<400> 75  
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<210> 76  
<211> 35  
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<400> 76  
tacgcgttgt gacatcgta tgacccagtc tccat 35

<210> 77  
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